

#8
Dmt
1-31-02RECEIVED
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1646

RAW SEQUENCE LISTING

DATE: 01/22/2002

PATENT APPLICATION: US/09/647,544

TIME: 14:51:51

Input Set : A:\003300-685.ST25.txt

Output Set: N:\CRF3\01222002\I647544.raw

PS

ENTERED

4 <110> APPLICANT: Lundgren-Akerlund, Evy
 6 <120> TITLE OF INVENTION: Integrin Heterodimer and a Subunit Thereof
 8 <130> FILE REFERENCE: 003300-685
 10 <140> CURRENT APPLICATION NUMBER: US 09/647,544
 11 <141> CURRENT FILING DATE: 2000-10-26
 13 <150> PRIOR APPLICATION NUMBER: PCT/SE99/00544
 14 <151> PRIOR FILING DATE: 1999-03-31
 16 <150> PRIOR APPLICATION NUMBER: SE 9801164-6
 17 <151> PRIOR FILING DATE: 1998-04-02
 19 <150> PRIOR APPLICATION NUMBER: SE 9900319.6
 20 <151> PRIOR FILING DATE: 1999-01-28
 22 <160> NUMBER OF SEQ ID NOS: 21
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 3884
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Human
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (22)...(3522)
 35 <400> SEQUENCE: 1
 36 cagggtcagaa accgatcagg c atg gaa ctc ccc ttc gtc act cac ctg ttc 51
 37 Met Glu Leu Pro Phe Val Thr His Leu Phe
 38 1 5 10
 40 ttg ccc ctg gtg ttc ctg aca ggt ctc tgc tcc ccc ttt aac ctg gat 99
 41 Leu Pro Leu Val Phe Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp
 42 15 20 25
 44 gaa cat cac cca cgc cta ttc cca ggg cca cca gaa gct gaa ttt gga 147
 45 Glu His His Pro Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly
 46 30 35 40
 48 tac agt gtc tta caa cat gtt ggg ggt gga cag cga tgg atg ctg gtg 195
 49 Tyr Ser Val Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val
 50 45 50 55
 52 ggc gcc ccc tgg gat ggg cct tca ggc gac cgg agg ggg gac gtt tat 243
 53 Gly Ala Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr
 54 60 65 70
 56 cgc tgc cct gta ggg ggg gcc cac aat gcc cca tgt gcc aag ggc cac 291
 57 Arg Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
 58 75 80 85 90
 60 tta ggt gac tac caa ctg gga aat tca tct cat cct gct gtg aat atg 339
 61 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn Met
 62 95 100 105
 64 cac ctg ggg atg tct ctg tta gag aca gat ggt gat ggg gga ttc atg 387

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65 His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly Phe Met
 66 110 115 120
 68 gcc tgt gcc cct ctc tgg tct cgt gct tgt ggc agc tct gtc ttc agt
 69 Ala Cys Ala Pro Leu Trp Ser Arg Ala Cys Gly Ser Ser Val Phe Ser
 70 125 130 135
 72 tct ggg ata tgt gcc cgt gtg gat gct tca ttc cag cct cag gga agc 483
 73 Ser Gly Ile Cys Ala Arg Val Asp Ala Ser Phe Gln Pro Gln Gly Ser
 74 140 145 150
 76 ctg gca ccc act gcc caa cgc tgc cca aca tac atg gat gtt gtc att 531
 77 Leu Ala Pro Thr Ala Gln Arg Cys Pro Thr Tyr Met Asp Val Val Ile
 78 155 160 165 170
 80 gtc ttg gat ggc tcc aac agc atc tac ccc tgg tct gaa gtt cag acc 579
 81 Val Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Ser Glu Val Gln Thr
 82 175 180 185
 84 ttc cta cga aga ctg gta ggg aaa ctg ttt att gac cca gaa cag ata 627
 85 Phe Leu Arg Arg Leu Val Gly Lys Leu Phe Ile Asp Pro Glu Gln Ile
 86 190 195 200
 88 cag gtg gga ctg gta cag tat ggg gag agc cct gta cat gag tgg tcc 675
 89 Gln Val Gly Leu Val Gln Tyr Gly Glu Ser Pro Val His Glu Trp Ser
 90 205 210 215
 92 ctg gga gat ttc cga acg aag gaa gaa gtg gtg aga gca gca aag aac 723
 93 Leu Gly Asp Phe Arg Thr Lys Glu Glu Val Val Arg Ala Ala Lys Asn
 94 220 225 230
 96 ctc agt cgg cgg gag gga cga gaa aca aag act gcc caa gca ata atg 771
 97 Leu Ser Arg Arg Glu Gly Arg Glu Thr Lys Thr Ala Gln Ala Ile Met
 98 235 240 245 250
 100 gtg gcc tgc aca gaa ggg ttc agt cag tcc cat ggg ggc cga ccc gag 819
 101 Val Ala Cys Thr Glu Gly Phe Ser Gln Ser His Gly Gly Arg Pro Glu
 102 255 260 265
 104 gct gcc agg cta ctg gtg gtt gtc act gat gga gag tcc cat gat gga 867
 105 Ala Ala Arg Leu Leu Val Val Val Thr Asp Gly Glu Ser His Asp Gly
 106 270 275 280
 108 gag gag ctt cct gca gca cta aag gcc tgt gag gct gga aga gtg aca 915
 109 Glu Glu Leu Pro Ala Ala Leu Lys Ala Cys Glu Ala Gly Arg Val Thr
 110 285 290 295
 112 cgc tat ggg att gca gtc ctt ggt cac tac ctc cgg cgg cag cga gat 963
 113 Arg Tyr Gly Ile Ala Val Leu Gly His Tyr Leu Arg Arg Gln Arg Asp
 114 300 305 310
 116 ccc agc tct ttc ctg aga gaa att aga act att gcc agt gat cca gat 1011
 117 Pro Ser Ser Phe Leu Arg Glu Ile Arg Thr Ile Ala Ser Asp Pro Asp
 118 315 320 325 330
 120 gag cga ttc ttc ttc aat gtc aca gat gag gct gct ctg act gac att 1059
 121 Glu Arg Phe Phe Phe Asn Val Thr Asp Glu Ala Ala Leu Thr Asp Ile
 122 335 340 345
 124 gtg gat gca cta gga gat cgg att ttt ggc ctt gaa ggg tcc cat gca 1107
 125 Val Asp Ala Leu Gly Asp Arg Ile Phe Gly Leu Glu Gly Ser His Ala
 126 350 355 360
 128 gaa aac gaa agc tcc ttt ggg ctg gaa atg tct cag att ggt ttc tcc 1155
 129 Glu Asn Glu Ser Ser Phe Gly Leu Glu Met Ser Gln Ile Gly Phe Ser

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130	365	370	375	
132	act cat cgg cta aag gat ggg att ctt ttt ggg atg gtg ggg gcc tat	1203		
133	Thr His Arg Leu Lys Asp Gly Ile Leu Phe Gly Met Val Gly Ala Tyr			
134	380 385 390			
136	gac tgg gga ggc tct gtg cta tgg ctt gaa gga ggc cac cgc ctt ttc	1251		
137	Asp Trp Gly Gly Ser Val Leu Trp Leu Glu Gly Gly His Arg Leu Phe			
138	395 400 405 410			
140	ccc cca cga atg gca ctg gaa gac gag ttc ccc cct gca ctg cag aac	1299		
141	Pro Pro Arg Met Ala Leu Glu Asp Glu Phe Gly Pro Pro Ala Leu Gln Asn			
142	415 420 425			
144	cat gca gcc tac ctg ggt tac tct gtt tct tcc atg ctt ttg cgg ggt	1347		
145	His Ala Ala Tyr Leu Gly Tyr Ser Val Ser Ser Met Leu Leu Arg Gly			
146	430 435 440			
148	gga cgc cgc ctg ttt ctc tct ggg gct cct cga ttt aga cat cga gga	1395		
149	Gly Arg Arg Leu Phe Leu Ser Gly Ala Pro Arg Phe Arg His Arg Gly			
150	445 450 455			
152	aaa gtc atc gcc ttc cag ctt aag aaa gat ggg gct gtg agg gtt gcc	1443		
153	Lys Val Ile Ala Phe Gln Leu Lys Lys Asp Gly Ala Val Arg Val Ala			
154	460 465 470			
156	cag agc ctc cag ggg gag cag att ggt tca tac ttt ggc agt gag ctc	1491		
157	Gln Ser Leu Gln Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Glu Leu			
158	475 480 485 490			
160	tgc cca ttg gat aca gat agg gat gga aca act gat gtc tta ctt gtg	1539		
161	Cys Pro Leu Asp Thr Asp Arg Asp Gly Thr Thr Asp Val Leu Leu Val			
162	495 500 505			
164	gct gcc ccc atg ttc ctg gga ccc cag aac aag gaa aca gga cgt gtt	1587		
165	Ala Ala Pro Met Phe Leu Gly Pro Gln Asn Lys Glu Thr Gly Arg Val			
166	510 515 520			
168	tat gtg tat ctg gta ggc cag cag tcc ttg ctg acc ctc caa gga aca	1635		
169	Tyr Val Tyr Leu Val Gly Gln Gln Ser Leu Leu Thr Leu Gln Gly Thr			
170	525 530 535			
172	ctt cag cca gaa ccc ccc cag gat gct cgg ttt ggc ttt gcc atg gga	1683		
173	Leu Gln Pro Glu Pro Pro Gln Asp Ala Arg Phe Gly Phe Ala Met Gly			
174	540 545 550			
176	gct ctt cct gat ctg aac caa gat ggt ttt gct gat gtg gct gtg ggg	1731		
177	Ala Leu Pro Asp Leu Asn Gln Asp Gly Phe Ala Asp Val Ala Val Gly			
178	555 560 565 570			
180	gcg cct ctg gaa gat ggg cac cag gga gca ctg tac ctg tac cat gga	1779		
181	Ala Pro Leu Glu Asp Gly His Gln Gly Ala Leu Tyr Leu Tyr His Gly			
182	575 580 585			
184	acc cag agt gga gtc agg ccc cat cct gcc cag agg att gct gct gcc	1827		
185	Thr Gln Ser Gly Val Arg Pro His Pro Ala Gln Arg Ile Ala Ala Ala			
186	590 595 600			
188	tcc atg cca cat gcc ctc agc tac ttt ggc cga agt gtg gat ggt cgg	1875		
189	Ser Met Pro His Ala Leu Ser Tyr Phe Gly Arg Ser Val Asp Gly Arg			
190	605 610 615			
192	cta gat ctg gat gga gat gat ctg gtc gat gtg gct gtg ggt gcc cag	1923		
193	Leu Asp Leu Asp Gly Asp Asp Leu Val Asp Val Ala Val Gly Ala Gln			
194	620 625 630			

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196	ggg	gca	gcc	atc	ctg	ctc	agc	tcc	cgg	ccc	att	gtc	cat	ctg	acc	cca	1971
197	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Ser	Arg	Pro	Ile	Val	His	Leu	Thr	Pro	
198	635					640				645						650	
200	tca	ctg	gag	gtg	acc	cca	cag	gcc	atc	agt	gtg	gtt	cag	agg	gac	tgt	2019
201	Ser	Leu	Glu	Val	Thr	Pro	Gln	Ala	Ile	Ser	Val	Val	Gln	Arg	Asp	Cys	
202					655					660						665	
204	agg	cgg	cga	ggc	caa	gaa	gca	gtc	tgt	ctg	act	gca	gcc	ctt	tgc	ttc	2067
205	Arg	Arg	Arg	Gly	Gln	Glu	Ala	Val	Cys	Leu	Thr	Ala	Ala	Leu	Cys	Phe	
206				670						675						680	
208	caa	gtg	acc	tcc	cgt	act	cct	ggt	cgc	tgg	gat	cac	caa	ttc	tac	atg	2115
209	Gln	Val	Thr	Ser	Arg	Thr	Pro	Gly	Arg	Trp	Asp	His	Gln	Phe	Tyr	Met	
210			685						690					695			
212	agg	ttc	acc	gca	tca	ctg	gat	gaa	tgg	act	gct	ggg	gca	cgt	gca	gca	2163
213	Arg	Phe	Thr	Ala	Ser	Leu	Asp	Glu	Trp	Thr	Ala	Gly	Ala	Arg	Ala	Ala	
214		700					705					710					
216	ttt	gat	ggc	tct	ggc	cag	agg	ttg	tcc	cct	cgg	agg	ctc	cgg	ctc	agt	2211
217	Phe	Asp	Gly	Ser	Gly	Gln	Arg	Leu	Ser	Pro	Arg	Arg	Leu	Arg	Leu	Ser	
218	715					720					725					730	
220	gtg	ggg	aat	gtc	act	tgt	gag	cag	cta	cac	ttc	cat	gtg	ctg	gat	aca	2259
221	Val	Gly	Asn	Val	Thr	Cys	Glu	Gln	Leu	His	Phe	His	Val	Leu	Asp	Thr	
222					735					740						745	
224	tca	gat	tac	ctc	cgg	cca	gtg	gcc	ttg	act	gtg	acc	ttt	gcc	ttg	gac	2307
225	Ser	Asp	Tyr	Leu	Arg	Pro	Val	Ala	Leu	Thr	Val	Thr	Phe	Ala	Leu	Asp	
226				750						755						760	
228	aat	act	aca	aag	cca	ggg	cct	gtg	ctg	aat	gag	ggc	tca	ccc	acc	tct	2355
229	Asn	Thr	Thr	Lys	Pro	Gly	Pro	Val	Leu	Asn	Glu	Gly	Ser	Pro	Thr	Ser	
230			765						770					775			
232	ata	caa	aag	ctg	gtc	ccc	ttc	tca	aag	gat	tgt	ggc	cct	gac	aat	gaa	2403
233	Ile	Gln	Lys	Leu	Val	Pro	Phe	Ser	Lys	Asp	Cys	Gly	Pro	Asp	Asn	Glu	
234		780					785					790					
236	tgt	gtc	aca	gac	ctg	gtg	ctt	caa	gtg	aat	atg	gac	atc	aga	ggc	tcc	2451
237	Cys	Val	Thr	Asp	Leu	Val	Leu	Gln	Val	Asn	Met	Asp	Ile	Arg	Gly	Ser	
238	795					800					805					810	
240	agg	aag	gcc	cca	ttt	gtg	gtt	cga	ggt	ggc	cgg	cgg	aaa	gtg	ctg	gta	2499
241	Arg	Lys	Ala	Pro	Phe	Val	Val	Arg	Gly	Gly	Arg	Arg	Lys	Val	Leu	Val	
242					815						820					825	
244	tct	aca	act	ctg	gag	aac	aga	aag	gaa	aat	gct	tac	aat	acg	agc	ctg	2547
245	Ser	Thr	Thr	Leu	Glu	Asn	Arg	Lys	Glu	Asn	Ala	Tyr	Asn	Thr	Ser	Leu	
246				830						835						840	
248	agt	atc	atc	ttc	tct	aga	aac	ctc	cac	ctg	gcc	agt	ctc	act	cct	cag	2595
249	Ser	Ile	Ile	Phe	Ser	Arg	Asn	Leu	His	Leu	Ala	Ser	Leu	Thr	Pro	Gln	
250			845							850						855	
252	aga	gag	agc	cca	ata	aag	gtg	gaa	tgt	gcc	gcc	cct	tct	gct	cat	gcc	2643
253	Arg	Glu	Ser	Pro	Ile	Lys	Val	Glu	Cys	Ala	Ala	Pro	Ser	Ala	His	Ala	
254		860								865						870	
256	cgg	ctc	tgc	agt	gtg	ggg	cat	cct	gtc	ttc	cag	act	gga	gcc	aag	gtg	2691
257	Arg	Leu	Cys	Ser	Val	Gly	His	Pro	Val	Phe	Gln	Thr	Gly	Ala	Lys	Val	
258	875					880					885					890	
260	acc	ttt	ctg	cta	gag	ttt	gag	ttt	agc	tgc	tcc	tct	ctc	ctg	agc	cag	2739

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261 Thr Phe Leu Leu Glu Phe Glu Phe Ser Cys Ser Ser Leu Leu Ser Gln
262      895      900      905
264 gtc ttt ggg aag ctg act gcc agc agt gac agc ctg gag aga aat ggc 2787
265 Val Phe Gly Lys Leu Thr Ala Ser Ser Asp Ser Leu Glu Arg Asn Gly
266      910      915      920
268 acc ctt caa gaa aac aca gcc cag acc tca gcc tac atc caa tat gag 2835
269 Thr Leu Gln Glu Asn Thr Ala Gln Thr Ser Ala Tyr Ile Gln Tyr Glu
270      925      930      935
272 ccc cac ctg ctc ctg ttc tct agt gag tct acc ctg cac cgc tat gag gtt 2883
273 Pro His Leu Leu Phe Ser Ser Glu Ser Thr Leu His Arg Tyr Glu Val
274      940      945      950
276 cac cca tat ggg acc ctc cca gtg ggt cct ggc cca gaa ttc aaa acc 2931
277 His Pro Tyr Gly Thr Leu Pro Val Gly Pro Gly Pro Glu Phe Lys Thr
278 955      960      965      970
280 act ctc agg gtt cag aac cta ggc tgc tat gtg gtc agt ggc ctc atc 2979
281 Thr Leu Arg Val Gln Asn Leu Gly Cys Tyr Val Val Ser Gly Leu Ile
282      975      980      985
284 atc tca gcc ctc ctt cca gct gtg gcc cat ggg ggc aat tac ttc cta 3027
285 Ile Ser Ala Leu Leu Pro Ala Val Ala His Gly Gly Asn Tyr Phe Leu
286      990      995      1000
288 tca ctg tct caa gtc atc act aac aat gca agc tgc ata gtg cag aac 3075
289 Ser Leu Ser Gln Val Ile Thr Asn Asn Ala Ser Cys Ile Val Gln Asn
290      1005      1010      1015
292 ctg act gaa ccc cca ggc cca cct gtg cat cca gag gag ctt caa cac 3123
293 Leu Thr Glu Pro Pro Gly Pro Pro Val His Pro Glu Glu Leu Gln His
294      1020      1025      1030
296 aca aac aga ctg aat ggg agc aat act cag tgt cag gtg gtg agg tgc 3171
297 Thr Asn Arg Leu Asn Gly Ser Asn Thr Gln Cys Gln Val Val Arg Cys
298 1035      1040      1045      1050
300 cac ctt ggg cag ctg gca aag ggg act gag gtc tct gtt gga cta ttg 3219
301 His Leu Gly Gln Leu Ala Lys Gly Thr Glu Val Ser Val Gly Leu Leu
302      1055      1060      1065
304 agg ctg gtt cac aat gaa ttt ttc cga aga gcc aag ttc aag tcc ctg 3267
305 Arg Leu Val His Asn Glu Phe Phe Arg Arg Ala Lys Phe Lys Ser Leu
306      1070      1075      1080
308 acg gtg gtc agc acc ttt gag ctg gga acc gaa gag ggc agt gtc cta 3315
309 Thr Val Val Ser Thr Phe Glu Leu Gly Thr Glu Glu Gly Ser Val Leu
310      1085      1090      1095
312 cag ctg act gaa gcc tcc cgt tgg agt gag agc ctc ttg gag gtg gtt 3363
313 Gln Leu Thr Glu Ala Ser Arg Trp Ser Glu Ser Leu Leu Glu Val Val
314      1100      1105      1110
316 cag acc cgg cct atc ctc atc tcc ctg tgg atc ctc ata ggc agt gtc 3411
317 Gln Thr Arg Pro Ile Leu Ile Ser Leu Trp Ile Leu Ile Gly Ser Val
318 1115      1120      1125      1130
320 ctg gga ggg ttg ctc ctg ctt gct ctc ctt gtc ttc tgc ctg tgg aag 3459
321 Leu Gly Gly Leu Leu Leu Ala Leu Leu Val Phe Cys Leu Trp Lys
322      1135      1140      1145
324 ctt ggc ttc ttt gcc cat aag aaa atc cct gag gaa gaa aaa aga gaa 3507
325 Leu Gly Phe Phe Ala His Lys Lys Ile Pro Glu Glu Glu Lys Arg Glu

```

Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:1021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15